

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 10/586,720
Source: 1 FWP
Date Processed by STIC: 7/31/06

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IFWP

RAW SEQUENCE LISTING

DATE: 07/31/2006

PATENT APPLICATION: US/10/586,720

TIME: 14:43:44

Input Set : A:\NEB-238-PUS.ST25.txt

Output Set: N:\CRF4\07312006\J586720.raw

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3 <110> APPLICANT: New England Biolabs, Inc.
4     Maina, Claude V.
5     Tzertzinis, George
6     Kumar, Sanjay
8 <120> TITLE OF INVENTION: Compositions and Methods for Generating Short
Double-Stranded RNA
9     Using Mutated RNase III
11 <130> FILE REFERENCE: NEB-238-PUS
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/586,720
C--> 13 <141> CURRENT FILING DATE: 2006-07-20
13 <150> PRIOR APPLICATION NUMBER: PCT/US05/02029
14 <151> PRIOR FILING DATE: 2005-01-21
16 <150> PRIOR APPLICATION NUMBER: 60/538,805
17 <151> PRIOR FILING DATE: 2004-01-23
19 <150> PRIOR APPLICATION NUMBER: 60/572,240
20 <151> PRIOR FILING DATE: 2004-05-18
22 <150> PRIOR APPLICATION NUMBER: 60/543,880
23 <151> PRIOR FILING DATE: 2004-02-12
25 <160> NUMBER OF SEQ ID NOS: 26
27 <170> SOFTWARE: PatentIn version 3.2
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 31
31 <212> TYPE: DNA
32 <213> ORGANISM: unknown
34 <220> FEATURE:
35 <223> OTHER INFORMATION: primer
37 <400> SEQUENCE: 1
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41 <210> SEQ ID NO: 2
42 <211> LENGTH: 36
43 <212> TYPE: DNA
44 <213> ORGANISM: unknown
46 <220> FEATURE:
47 <223> OTHER INFORMATION: primer
49 <400> SEQUENCE: 2
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54 <211> LENGTH: 26
55 <212> TYPE: DNA
56 <213> ORGANISM: unknown
58 <220> FEATURE:
59 <223> OTHER INFORMATION: primer
61 <400> SEQUENCE: 3
62 cagtaaacad aacgcgcgtt tagaat                                     26

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67 <212> TYPE: DNA
68 <213> ORGANISM: unknown
70 <220> FEATURE:
71 <223> OTHER INFORMATION: primer
73 <400> SEQUENCE: 4
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77 <210> SEQ ID NO: 5
78 <211> LENGTH: 31
79 <212> TYPE: DNA
80 <213> ORGANISM: unknown
82 <220> FEATURE:
83 <223> OTHER INFORMATION: primer
85 <400> SEQUENCE: 5
86 ctcggtgtgga tgcaggcgat atgagccgga t        31
89 <210> SEQ ID NO: 6
90 <211> LENGTH: 33
91 <212> TYPE: DNA
92 <213> ORGANISM: unknown
94 <220> FEATURE:
95 <223> OTHER INFORMATION: primer
97 <400> SEQUENCE: 6
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101 <210> SEQ ID NO: 7
102 <211> LENGTH: 20
103 <212> TYPE: DNA
104 <213> ORGANISM: unknown
106 <220> FEATURE:
107 <223> OTHER INFORMATION: primer
109 <400> SEQUENCE: 7
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113 <210> SEQ ID NO: 8
114 <211> LENGTH: 38
115 <212> TYPE: DNA
116 <213> ORGANISM: unknown
118 <220> FEATURE:
119 <223> OTHER INFORMATION: primer
121 <400> SEQUENCE: 8
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125 <210> SEQ ID NO: 9
126 <211> LENGTH: 225
127 <212> TYPE: PRT
128 <213> ORGANISM: unknown
130 <220> FEATURE:
131 <223> OTHER INFORMATION: relevant region from Pasteurella multocida
133 <400> SEQUENCE: 9
135 Met Thr Gln Asn Leu Glu Arg Leu Gln Arg Gln Ile Gly Tyr Gln Phe
136 1          5          10          15

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139 Asn Gln Pro Ala Leu Leu Lys Gln Ala Leu Thr His Arg Ser Ala Ala
140           20           25           30
143 Val Lys His Asn Glu Arg Leu Glu Phe Leu Gly Asp Ala Ile Leu Asn
144           35           40           45
147 Phe Ile Ile Ala Glu Ala Leu Tyr His Gln Phe Pro Lys Cys Asn Glu
148           50           55           60
151 Gly Glu Leu Ser Arg Met Arg Ala Thr Leu Val Arg Glu Pro Thr Leu
152 65           70           75           80
155 Ala Ser Leu Ala Arg Gln Phe Glu Leu Gly Asp Tyr Leu Ser Leu Gly
156           85           90           95
159 Pro Gly Glu Leu Lys Ser Gly Gly Phe Arg Arg Glu Ser Ile Leu Ala
160           100          105          110
163 Asp Cys Val Glu Ala Ile Ile Gly Ala Ile Ser Leu Asp Ser Asp Leu
164           115          120          125
167 Ala Thr Thr Thr Lys Ile Val Gln His Trp Tyr Gln Ala Gln Leu Lys
168           130          135          140
171 Gln Ile Gln Pro Gly Asp Asn Gln Lys Asp Pro Lys Thr Arg Leu Gln
172 145          150          155          160
175 Glu Tyr Leu Gln Gly Lys Arg Leu Pro Leu Pro Thr Tyr Asn Val Val
176           165          170          175
179 Glu Ile Lys Gly Glu Ala His Cys Gln Thr Phe Thr Val Glu Cys Tyr
180           180          185          190
183 Val Lys Asn Ile Asp Arg Thr Phe Met Gly Ser Gly Ala Ser Arg Arg
184           195          200          205
187 Lys Ala Glu Gln Ala Ala Ala Glu Lys Ile Leu Gln Leu Leu Glu Met
188           210          215          220
191 Lys
192 225
195 <210> SEQ ID NO: 10
196 <211> LENGTH: 227
197 <212> TYPE: PRT
198 <213> ORGANISM: unknown
200 <220> FEATURE:
201 <223> OTHER INFORMATION: relevant region from H. Influenzae
203 <400> SEQUENCE: 10
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209 Asp Ile Ala Leu Leu Lys Gln Ala Leu Thr His Arg Ser Ala Ala Thr
210           20           25           30
213 Gln His Asn Glu Arg Leu Glu Phe Leu Gly Asp Ser Ile Leu Asn Phe
214           35           40           45
217 Thr Ile Ala Glu Ala Leu Tyr His Gln Phe Pro Arg Cys Asn Glu Gly
218           50           55           60
221 Glu Leu Ser Arg Met Arg Ala Thr Leu Val Arg Glu Pro Thr Leu Ala
222 65           70           75           80
225 Ile Leu Ala Arg Gln Phe Glu Leu Gly Asp Tyr Met Ser Leu Gly Ser
226           85           90           95
229 Gly Glu Leu Lys Asn Gly Gly Phe Arg Arg Glu Ser Ile Leu Ala Asp
230           100          105          110

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233 Cys Val Glu Ala Ile Ile Gly Ala Met Ser Leu Asp Gln Gly Leu Ala
234      115      120      125
237 Val Thr Thr Gln Val Ile Arg Asn Trp Tyr Gln Gln Leu Leu Ala Glu
238      130      135      140
241 Ile Lys Pro Gly Asp Asn Gln Lys Asp Ala Lys Thr Arg Leu Gln Glu
242 145      150      155      160
245 Tyr Leu Gln Gly Lys His Leu Pro Leu Pro Thr Tyr Glu Val Val Asn
246      165      170      175
249 Ile Gln Gly Glu Ala His Cys Gln Ile Phe Thr Val Lys Cys Lys Val
250      180      185      190
253 Lys Ser Ala Glu Lys Ile Asp Arg Thr Phe Val Ala Lys Gly Ser Ser
254      195      200      205
257 Arg Arg Lys Ala Glu Gln Ala Ala Ala Glu Gln Ile Leu Lys Glu Leu
258      210      215      220
261 Asp Ile Lys
262 225
265 <210> SEQ ID NO: 11
266 <211> LENGTH: 224
267 <212> TYPE: PRT
268 <213> ORGANISM: unknown
270 <220> FEATURE:
271 <223> OTHER INFORMATION: relevant region from S. typhimurium
273 <400> SEQUENCE: 11
275 Met Asn Pro Ile Val Ile Asn Arg Leu Gln Arg Lys Leu Gly Tyr Thr
276 1      5      10      15
279 Phe Asn His Gln Glu Leu Leu Gln Gln Ala Leu Thr His Arg Ser Ala
280      20      25      30
283 Ser Ser Lys His Asn Glu Arg Leu Glu Phe Leu Gly Asp Ser Ile Leu
284      35      40      45
287 Ser Phe Val Ile Ala Asn Ala Leu Ser Arg Phe Pro Arg Val Asp Glu
288      50      55      60
291 Gly Asp Met Ser Arg Met Arg Asp Pro Leu Val Arg Gly Asn Thr Leu
292 65      70      75      80
295 Ala Glu Leu Ala Arg Glu Phe Asp Leu Gly Glu Cys Leu Arg Leu Gly
296      85      90      95
299 Pro Gly Glu Leu Lys Ser Gly Gly Phe Arg Arg Glu Ser Ile Leu Ala
300      100     105     110
303 Asp Thr Val Glu Ala Leu Ile Gly Gly Val Phe Leu Asp Ser Asn Ile
304      115     120     125
307 Gln Thr Val Glu Gln Leu Ile Leu Asn Trp Tyr Lys Thr Arg Leu Asp
308      130     135     140
311 Glu Ile Ser Pro Gly Asp Lys Gln Lys Asp Pro Lys Thr Arg Leu Gln
312 145     150     155     160
315 Glu Tyr Leu Gln Gly Arg His Leu Pro Leu Pro Ser Tyr Leu Val Val
316      165     170     175
319 Gln Val Arg Gly Glu Ala His Asp Gln Glu Phe Thr Ile His Cys Gln
320      180     185     190
323 Val Ser Gly Leu Ser Glu Pro Val Val Gly Thr Gly Ser Ser Arg Arg
324      195     200     205

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327 Lys Ala Glu Gln Ala Ala Ala Asn Ser Val Lys Lys Leu Glu Leu Glu
328      210                      215                      220
331 <210> SEQ ID NO: 12
332 <211> LENGTH: 226
333 <212> TYPE: PRT
334 <213> ORGANISM: unknown
336 <220> FEATURE:
337 <223> OTHER INFORMATION: relevant region from E. coli
339 <400> SEQUENCE: 12
341 Met Asn Pro Ile Val Ile Asn Arg Leu Gln Arg Lys Leu Gly Tyr Thr
342 1          5          10          15
345 Phe Asn His Gln Glu Leu Leu Gln Gln Ala Leu Thr His Arg Ser Ala
346      20          25          30
349 Ser Ser Lys His Asn Glu Arg Leu Glu Phe Leu Gly Asp Ser Ile Leu
350      35          40          45
353 Ser Tyr Val Ile Ala Asn Ala Leu Tyr His Arg Phe Pro Arg Val Asp
354      50          55          60
357 Glu Gly Asp Met Ser Arg Met Arg Ala Thr Leu Val Arg Gly Asn Thr
358 65          70          75          80
361 Leu Ala Glu Leu Ala Arg Glu Phe Glu Leu Gly Glu Cys Leu Arg Leu
362      85          90          95
365 Gly Pro Gly Glu Leu Lys Ser Gly Gly Phe Arg Arg Glu Ser Ile Leu
366      100         105         110
369 Ala Asp Thr Val Glu Ala Leu Ile Gly Gly Val Phe Leu Asp Ser Asp
370      115         120         125
373 Ile Gln Thr Val Glu Lys Leu Ile Leu Asn Trp Tyr Gln Thr Arg Leu
374      130         135         140
377 Asp Glu Ile Ser Pro Gly Asp Lys Gln Lys Asp Pro Lys Thr Arg Leu
378 145         150         155         160
381 Gln Glu Tyr Leu Gln Gly Arg His Leu Pro Leu Pro Thr Tyr Leu Val
382      165         170         175
385 Val Gln Val Arg Gly Glu Ala His Asp Gln Glu Phe Thr Ile His Cys
386      180         185         190
389 Gln Val Ser Gly Leu Ser Glu Pro Val Val Gly Thr Gly Ser Ser Arg
390      195         200         205
393 Arg Lys Ala Glu Gln Ala Ala Glu Gln Ala Leu Lys Lys Leu Glu
394      210         215         220
397 Leu Glu
398 225
401 <210> SEQ ID NO: 13
402 <211> LENGTH: 225
403 <212> TYPE: PRT
404 <213> ORGANISM: unknown
406 <220> FEATURE:
407 <223> OTHER INFORMATION: relevant region from V. cholerae
409 <400> SEQUENCE: 13
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415 Lys Glu Thr Glu Leu Leu Asn Leu Ala Leu Thr His Arg Ser Ala Asn

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VERIFICATION SUMMARY

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Input Set : A:\NEB-238-PUS.ST25.txt

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date